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RAW SEQUENCE LISTING

DATE: 06/27/2003

PATENT APPLICATION: US/09/825,012A

TIME: 08:38:32

Input Set : A:\Sequence.txt

Output Set: N:\CRF4\06272003\I825012A.raw

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3 <110> APPLICANT: Young, Robert
5 <120> TITLE OF INVENTION: Compounds for Targeting
7 <130> FILE REFERENCE: 43191-256808
9 <140> CURRENT APPLICATION NUMBER: US 09/825,012A
10 <141> CURRENT FILING DATE: 2001-04-03
12 <150> PRIOR APPLICATION NUMBER: US 60/237,159
13 <151> PRIOR FILING DATE: 2000-10-02
15 <150> PRIOR APPLICATION NUMBER: GB 0008049.9
16 <151> PRIOR FILING DATE: 2000-04-03
18 <160> NUMBER OF SEQ ID NOS: 101
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 282
24 <212> TYPE: PRT
25 <213> ORGANISM: Homo sapiens
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33 Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr
34 20 25 30
37 Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val
38 35 40 45
41 Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp
42 50 55 60
45 Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp
46 65 70 75 80
49 Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn
50 85 90 95
53 Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
54 100 105 110
57 Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
58 115 120 125
61 Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe
62 130 135 140
65 Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly
66 145 150 155 160
69 Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val
70 165 170 175
73 Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn
74 180 185 190
77 Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu
78 195 200 205
81 Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr

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82      210      215      220
85 Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
86 225      230      235      240
89 Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn
90      245      250      255
93 Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser
94      260      265      270
97 Asp His Tyr Pro Val Glu Val Met Leu Lys
98      275      280
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102 <211> LENGTH: 1039
103 <212> TYPE: DNA
104 <213> ORGANISM: Homo sapiens
106 <400> SEQUENCE: 2
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109 ttttctttaa gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag      120
111 cattctcgtc atctctgagg acatcaccat catctcagga tgaggggcat gaagctgctg      180
113 ggggcgctgc tggcactggc ggccctactg cagggggccg tgtccctgaa gatcgagcc      240
115 ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt      300
117 gtgcagatcc tgagccgcta tgacatgcc ctggtccagg aggtcagaga cagccacctg      360
119 actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac      420
121 gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg      480
123 cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg      540
125 aacgacacct tcaaccgaga gccagccatt gtcaggttct tctcccgtt cacagaggtc      600
127 agggagtttg ccattgttcc cctgcatgcg gcccggggg acgcagtagc cgagatcgac      660
129 gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttggagga cgtcatgttg      720
131 atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc      780
133 ctgtggacaa gcccacctt ccagtggctg atccccgaca gcgctgacac cacagctaca      840
135 cccacgcact gtgcctatga caggatcgct gttgcaggga tgctgctccg aggcgccgtt      900
137 gttcccgact cggctcttcc cttaaacttc caggctgcct atggcctgag tgaccaactg      960
139 gcccaagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtgagc agcccctccc      1020
141 cacaccagtt gaactgcag      1039
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145 <211> LENGTH: 260
146 <212> TYPE: PRT
147 <213> ORGANISM: Homo sapiens
149 <400> SEQUENCE: 3
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152 1      5      10      15
155 Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr
156      20      25      30
159 Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val
160      35      40      45
163 Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His
164      50      55      60
167 Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr
168 65      70      75      80
171 Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr Tyr
172      85      90      95

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175 Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg Glu
176          100          105          110
179 Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu Phe
180          115          120          125
183 Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile
184          130          135          140
187 Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu
188 145          150          155          160
191 Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val
192          165          170          175
195 Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe
196          180          185          190
199 Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr His
200          195          200          205
203 Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala
204          210          215          220
207 Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly
208 225          230          235          240
211 Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu
212          245          250          255
215 Val Met Leu Lys
216          260
219 <210> SEQ ID NO: 4
220 <211> LENGTH: 783
221 <212> TYPE: DNA
222 <213> ORGANISM: Homo sapiens
224 <400> SEQUENCE: 4
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227 ctcgtcagct acattgtgca gatcctgagc cgctacgaca tcgccctggt ccaggaggtc      120
229 agagacagcc acctgactgc cgtggggaag ctgctggaca acctcaatca ggacgcacca      180
231 gacacctatc actacgtggt cagttagcca ctgggacgga acagctataa ggagcgctac      240
233 ctgttcgtgt acaggcctga ccagggtgtc gcggtggaca gctactacta cgatgatggc      300
235 tgcgagccct gcgggaacga caccttcaac cgagagccag ccattgtcag gttcttctcc      360
237 cggttcacag aggtcaggga gtttgccatt gttccctgc atgcggcccc gggggacgca      420
239 gtagccgaga tcgacgtctc ctatgacgtc tacctggatg tccaagagaa atggggcttg      480
241 gaggacgtca tgttgatggg cgacttcaat gcgggctgca gctatgtgag accctcccag      540
243 tggatcatcca tccgctgtg gacaagcccc accttcagtg ggctgatccc cgacagcgct      600
245 gacaccacag ctacaccac gactgtgcc tatgacagga tcgtggttgc agggatgctg      660
247 ctccgagggg ccgttgttcc cgactcggct ctcccttta acttcaggc tgcctatggc      720
249 ctgagtgacc aactggccca agccatcagt gaccactatc cagtggaggt gatgctgaag      780
251 tga
254 <210> SEQ ID NO: 5
255 <211> LENGTH: 161
256 <212> TYPE: PRT
257 <213> ORGANISM: Homo sapiens
259 <400> SEQUENCE: 5
261 Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu
262 1          5          10          15
265 Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr

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266          20          25          30
269 Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val
270          35          40          45
273 Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp
274          50          55          60
277 Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp
278 65          70          75          80
281 Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn
282          85          90          95
285 Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
286          100          105          110
289 Ala Val Asp Ser Tyr Tyr Tyr Asp Gly Cys Glu Pro Cys Gly Asn
290          115          120          125
293 Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe
294          130          135          140
297 Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly
298 145          150          155          160
301 Asp
305 <210> SEQ ID NO: 6
306 <211> LENGTH: 858
307 <212> TYPE: DNA
308 <213> ORGANISM: Homo sapiens
310 <400> SEQUENCE: 6
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313 cagggggccg tgtccctgaa gatcgagcc ttcaacatcc agacatttgg ggagaccaag 120
315 atgtccaatg ccaccctcgt cagctacatt gtgcagatcc tgagccgcta cgacatcgcc 180
317 ctggtccagg aggtcagaga cagccacctg actgcctggt ggaagctgct ggacaacctc 240
319 aatcaggacg caccagacac ctatcactac gtggtcagtg agccactggg acggaacagc 300
321 tataaggagc gctacctgtt cgtgtacagg cctgaccagg tgtctgcggt ggacagctac 360
323 tactacgatg atggctgcga gccctgcggg aacgacacct tcaaccgaga gccagccatt 420
325 gtcaggttct tctcccgtt cacaagaggtc agggagtgtt ccattgttcc cctgcatgcg 480
327 gccccggggg acgcagtagc cgagatcgac gctctctatg acgtctacct ggatgtccaa 540
329 gagaaatggg gcttgaggga cgtcatgttg atgggcgact tcaatgcggg ctgcagctat 600
331 gtgagaccct ccagtggtc atccatccgc ctgtggacaa gccccacctt ccagtggctg 660
333 atccccgaca gcgctgacac cacagctaca ccaacgcact gtgcctatga caggatcgctg 720
335 gttgcaggga tgctgctccg aggggcctgt gttcccgaact cggctcttcc ctttaacttc 780
337 caggtgcct atggcctgag tgaccaactg gccaagcca tcagtgacca ctatccagtg 840
339 gagtgatgc tgaagtga
342 <210> SEQ ID NO: 7
343 <211> LENGTH: 721
344 <212> TYPE: DNA
345 <213> ORGANISM: Artificial Sequence
347 <220> FEATURE:
348 <223> OTHER INFORMATION: Humanised HMFG-1 light chain
350 <400> SEQUENCE: 7
351 atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt ccaactccgac 60
353 atccagatga cccagagccc aagcagcctg agcgccagcg tgggtgacag agtgaccatc 120
355 acctgtaagt ccagtcagag ccttttatat agtagcaatc aaaagatcta cttggcctgg 180
357 taccagcaga agccaggtaa ggctccaaag ctgctgatct actgggcata cactagggaa 240

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359 tctggtgtgc caagcagatt cagcggtagc ggtagcggta ccgacttcac cttcaccatc 300
361 agcagcctcc agccagagga catcgccacc tactactgcc agcaatatta tagatatcct 360
363 cggacgttcg gccaaaggac caaggtggaa atcaaacgaa ctgtggctgc accatctgtc 420
365 ttcattctcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 480
367 ctgaataact tctatcccag agaggccaaa gtacagtggg aggtggataa cgccctccaa 540
369 tcgggttaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 600
371 agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgctgcgaa 660
373 gtcacccatc agggcctgag ctgcgccgtc acaaagagct tcaacagggg agagtgttag 720
375 a 721

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378 <210> SEQ ID NO: 8

379 <211> LENGTH: 730

380 <212> TYPE: DNA

381 <213> ORGANISM: Artificial Sequence

383 <220> FEATURE:

384 <223> OTHER INFORMATION: Humanised HMFG-1 light chain

386 <400> SEQUENCE: 8

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387 gccgccacca tgggatggag ctgtatcatc ctcttcttgg tagcaacagc tacagggtgc 60
389 cactccgaca tccagatgac ccagagccca agcagcctga gcgccagcgt gggtgacaga 120
391 gtgaccatca cctgtaagtc cagtcagagc cttttatata gtagcaatca aaagatctac 180
393 ttggcctggt accagcagaa gccaggtaag gtcctaaagc tgctgatcta ctgggcatcc 240
395 actagggaa ctggtgtgcc aagcagattc agcggtagcg gtagcggtag cgacttcacc 300
397 ttcaccatca gcagcctcca gccagaggac atcgccacct actactgcca gcaatattat 360
399 agatatcctc ggacgttcgg ccaagggacc aaggtggaaa tcaaacgaac tgtggctgca 420
401 ccatctgtct tcatcttccc gccatctgat gagcagttga aatctggaac tgcctctgtt 480
403 gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac 540
405 gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc 600
407 tacagcctca gcagcacctc gacgctgagc aaagcagact acgagaaaca caaagtctac 660
409 gcctgcgaag tcacccatca gggcctgagc tcgcccgtca caaagagctt caacagggga 720
411 gagtggttaga 730

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414 <210> SEQ ID NO: 9

415 <211> LENGTH: 239

416 <212> TYPE: PRT

417 <213> ORGANISM: Artificial Sequence

419 <220> FEATURE:

420 <223> OTHER INFORMATION: Humanised HMFG-1 light chain

422 <400> SEQUENCE: 9

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424 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
425 1 5 10 15
428 Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
429 20 25 30
432 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu
433 35 40 45
436 Leu Tyr Ser Ser Asn Gln Lys Ile Tyr Leu Ala Trp Tyr Gln Gln Lys
437 50 55 60
440 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
441 65 70 75 80
444 Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
445 85 90 95
448 Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr

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VERIFICATION SUMMARY

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Input Set : A:\Sequence.txt

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L:1920 M:258 W: Mandatory Feature missing, <223> Blank for, SEQ#:45,Line#:1917
L:2398 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:48,Line#:2395
L:2876 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:51,Line#:2873
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